



# New Perspectives on Defeating Multidrug Resistant Bacteria

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## Introduction

According to Austin (2001) understanding the spread of antibiotic resistant pathogens in hospitals is vitally important. As the time goes on more and more microorganisms are becoming drug resistant and it is becoming increasingly important to find a method to control that. Having said that, it is important to note that this article was written more than 10 years ago and still a way to control microorganisms has not been found showing an even greater need to find a way to control the microorganisms from becoming immune to all the drugs.

In this research I will be studying the microorganisms closely and evaluating the multidrug resistance in bacteria to find out if there is a particular mechanism all the bacteria use to become resistant. For the mechanism I will be focusing on the chromosomal mechanism of the bacteria, in particular the gram-negative bacteria.

If I am able to find a particular mechanism that all the bacteria use then it can become easier to find a drug that targets that and would lead to the prevention of microorganisms' immunity.

## Research Question

There are many factors that play a role in a bacteria becoming multidrug resistant. Knowing that, in this research I want to look at the chromosomal mechanism of the bacteria as it becomes resistant a drug or many different type of drugs.

My research question is whether there is one certain type of mechanism or part of the mechanism that can be followed in all the different type of bacteria.

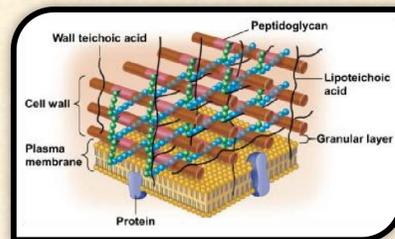


Figure 1: shows the gram-positive bacteria

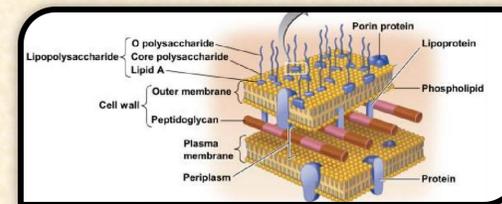


Figure 2: shows the gram-negative bacteria

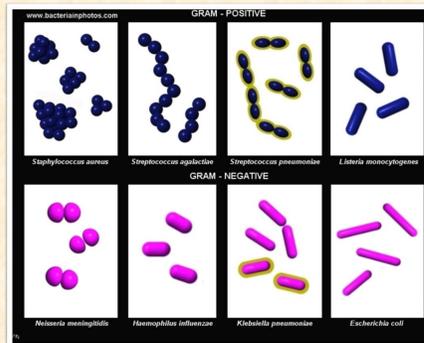


Figure 3: shows the gram-positive bacteria and the gram-negative bacteria with their shape and the organization

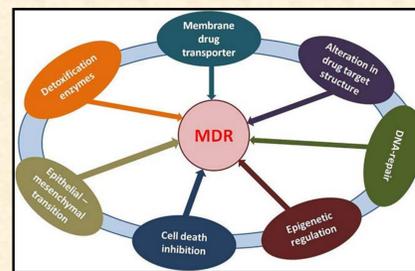


Figure 5: This shows the different factors that play a role in a bacteria becoming multidrug resistant.

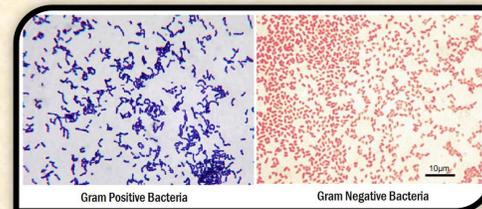


Figure 4: shows the gram-positive and gram-negative bacteria after they are gram stained.

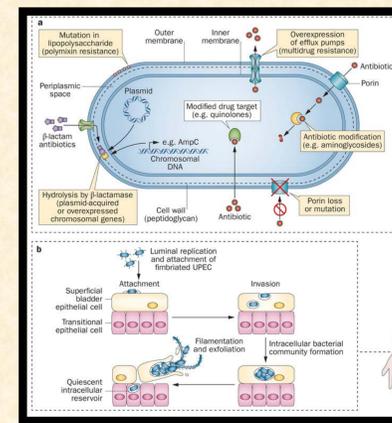


Figure 6: An example of a mechanism is shown.

## Significance and Conclusion

I expect my work will show that there are multiple factors that play a role in a bacteria becoming multidrug resistant, but there is a common mechanism that they all follow.

This will provide a new direction that can then be used to further the study and find a way to stop multidrug resistance. The information can then be used to make certain drugs or other treatments. Medicine would then be targeted at that particular chromosomal mechanism.

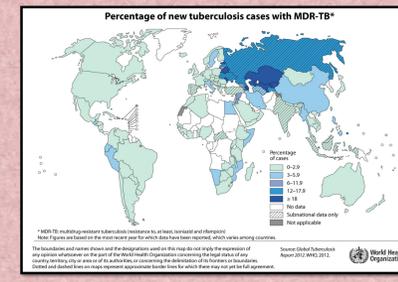


Figure 7: Shows the cases of multidrug resistant TBR in the world. Showing the importance and need to find a new method of fighting multidrug resistance.

Figure 8: shows a list of different bacteria and how within those bacteria there are already multidrug resistance strains.

Organism	Total isolates*	No. of MDR clusters (no. of isolates)	No. of sites with MDR clusters	No. of clusters with possible clonal spread (no. of isolates)†	No. of sites with MDR clones
Staphylococcus aureus	2348	49 (250)	34	35 (145)	28
Klebsiella pneumoniae	677	14 (51)	12	8 (20)	7
Escherichia coli	1755	14 (53)	10	6 (22)	6
Enterococcus faecium	157	4 (11)	4	2 (7)	2
Acinetobacter baumannii	125	4 (12)	3	2 (6)	2
Pseudomonas aeruginosa	477	3 (12)	3	3 (7)	3
Enterobacter aerogenes	84	2 (9)	2	2 (4)	2
Enterobacter cloacae	265	1 (4)	1	1 (3)	1
Stenotrophomonas maltophilia	64	1 (3)	1	1 (2)	1
Proteus mirabilis	140	1 (3)	1	1 (2)	1
Streptococcus pneumoniae	455	1 (3)	1	1 (2)	1
Total	6547	94 (410)	44*	62 (218)	33†

\* Total number of isolates of each species tested in objective A, 1999 (from the United States, Canada, Latin America, Europe, Israel and Turkey; total of 72 study sites).  
† Possible clonal spread is defined as isolates with identical ribotypes and pulsed-field gel electrophoresis profiles. Source: [http://www.who.int/tb/diagnosis/20050513/figure/Fig4A3\\_32480707734648145\\_445143042/Tab4-4-Molecular-analysis-of-organisms-exhibiting-multi-drug-resistance-MDR.png](http://www.who.int/tb/diagnosis/20050513/figure/Fig4A3_32480707734648145_445143042/Tab4-4-Molecular-analysis-of-organisms-exhibiting-multi-drug-resistance-MDR.png)

## Background

### Drug resistance or Multidrug resistance:

is when a bacteria that was once dying from the use of a particular drug no longer is affected by that drug. This means it becomes resistant to drugs and this problem increases when it becomes resistant to not one drug, but multiple drugs.

### Gram-negative:

are those organisms that do not have the thick layer of peptidoglycan cell wall. Some of the gram-negative bacteria cases include things like bloodstream infections, pneumonia, etc.

### Gram-positive:

bacteria are those that do have a thick layer of peptidoglycan in the cell wall with membrane layer above it.

### Peptidoglycan:

Mostly found in the cell walls of the gram-positive and gram-negative bacteria which has polymer that are made of the polysaccharide chains and the peptide chains. This is also called mucopolysaccharide or murein.

## Methods

I am going to work with two different types of bacteria that are multidrug resistant, compare their chromosomal mechanisms, and use that data to determine if it is possible that all bacteria use the same mechanism.

I will choose two bacteria that are resistant to the same drugs and follow that with library research to find out if a chromosomal mechanism that makes the organisms resistant and then compare the mechanisms of both.

By comparing the two mechanisms I will be able to see if at any particular point the mechanisms are similar and if we can target that similarity.

## Rationale

In this research, I plan to work with bacteria that are multidrug resistant. By doing this, I want to find if all the bacteria have the same mechanism that leads to resistance and, if I find the mechanisms to be the same, then that information can lead us to better understand how to stop the rising problem of bacteria becoming resistant to drugs. Along with that, I want to know if genetics play a role; for example, whether the same site of the chromosome is affected by the mutations that occur or if it is a mutation that happens randomly at any chromosome on any location.

## Works Cited

- Austin, D., & Lipsitch, M. (2001). Understanding the spread of antibiotic resistant pathogens in hospitals: mathematical models as tools for control. *Clinical Infectious Diseases*, 33(10), 1739-1746.
- Dye, C., Williams, B., Espinal, M., & Ravignone, M. (2002). Erasing the world's slow stain: strategies to beat multidrug-resistant tuberculosis. *Science*, 295(5562), 2042-2046.
- Healthcare-associated Infections. (2011, January 17). Retrieved April 26, 2017, from <https://www.cdc.gov/hai/organisms/gram-negative-bacteria.html>
- Hosam M. Z, Harris, P. N. A., Roberts, M. J., Tambyah, P. A., Schembri, M. A., Pezzani, M. D., Williamson, D. A., & Paterson D. L. (2015). The emerging threat of multidrug-resistant gram-negative bacteria in urology. *Nature Reviews Urology*, 12, 570-584.
- Kaufman, G., & Kaufman, (2011). Antibiotics: mode of action and mechanisms of resistance. *Nursing Standard*, 25(42), 49.
- Medical Definition of Antibiotic resistance. (n.d.). Retrieved May 10, 2017, from <http://www.medicinenet.com/script/main/art.asp?articlekey=2276>
- Nikaido, H. (2009). Multidrug resistance in bacteria. *Annual Review of Biochemistry*, 78, 119.
- Peptidoglycan. (n.d.). Retrieved May 12, 2017, from <https://www.merriam-webster.com/dictionary/peptidoglycan>
- Tortora, G. J., Funke, B. R., & Case, C. L. (2016). *Microbiology: an introduction*. Boston: Pearson.

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